

5'	CT	AAC	TTT	GGC	CTG	GGA	CTC	TGC	CCC	TCT	ACC	TCA	GCA	CAG	AAT	CGC	CCC	GGG
			9			18			27			36			45		54	
	TCC	TAC	TAC	AGA	ATC	AAT	CCT	TGA	ACA	CTG	CCT	CCA	CGT	CGC	CGG	CTC	AAT	CTG
			63			72			81			90			99		108	
	GGC	GAG	AAC	CCA	GAC	TTC	CAC	CGC	AGC	CCC	GCA	ATC	TGC	AGA	CCT	CAG	CGG	CAG
						117			126			135			144		162	
	CGC	AGG	TGG	CAG	ACC	TGC	CTC	CTT	TGC	CTG	TGA	GTC	ATG	GCA	GCT	CCC	ATG	AAT
						171			180			189			198		216	
	GGC	CAA	GTC	TGT	GTC	GTC	ACT	GGT	GCC	TCC	AGG	GGT	ATT	GGC	CGT	GGC	ATT	GCC
						225			234			243			252		270	
	TTC	CAG	CTC	TGC	AAA	GCA	GGC	GCC	ACA	GTT	TAC	ATC	ACT	GGC	CGC	CAT	CTG	GAC
						279			288			297			306		324	
	ACC	CTT	CGC	GTT	GTT	GCT	CAG	GAG	GCA	CAA	TCC	CTC	GGG	GGC	CAA	TGT	GTG	CCT
						333			342			351			360		378	

Figure 1A

387	396	405	414	423	432
GTG GTG TGC GAT TCA AGC CAG GAG AGT GAA GTG CGA ACG CTG TTT GAG CAA GTG					
V V C D S S Q E S E V R T L F E Q V					
441	450	459	468	477	486
GAT CGG GAA CAG CAA GGG CGT CTA GAT GTG CTG GTC AAC AAT GCT TAT GCA GGG					
D R E Q Q G G R L D V L V N N A Y A G					
495	504	513	522	531	540
GTC CAG ACG ATC CTG AAC ACC AGG AAT AAG GCA TTC TGG GAA ACC CCT GCC TCC					
V Q T I L N T R N K A F W E T P A S					
549	558	567	576	585	594
ATG TGG GAT GAT ATC AAC AAC GTC GGA CTC AGA GGC CAC TAC TTT TGC TCA GTG					
M W D D I N N V G L R G H Y F C S V					
603	612	621	630	639	648
TAT GGG GCA CGG CTG ATG GTA CCA GCT GGC CAG GGG CTC ATC GTG GTC ATC TCC					
Y G A R L M V P A G Q G L I V V I S					
657	666	675	684	693	702
TCC CCA GGA AGC CTG CAG TAT ATG TTC AAT GTC CCC TAT GGT GTG GGC AAA GCT					
S P G S L Q Y M F N V P Y G V G K A					

Figure 1B

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711	GGG TGT GAC AAG CTG GCT GCT GAC TGT GCC CAC GAG CTG CGG CGC CAT GGG GTC	720	729	738	747	756
A C D K L A A D C A H E L R R H G V						
765	AGC TGT CTG TCT CTG TGG CCG GGG ATT GTG CAG ACA GAA CTG CTG AAG GAG CAT	774	783	792	801	810
S C V S L W P G I V Q T E L L K E H						
819	ATG GCA AAG GAG GAG GTC CTG CAG GAT CCT GTG TTG AAG CAG TTC AAA TCA GCC	828	837	846	855	864
M A K E E V L Q D P V L K Q F K S A						
873	TTC TCA TCT GCA GAA ACC ACA GAA TTG AGT GGC AAA TGT GTG GTG GCT TTG GCA	882	891	900	909	918
F S S A E T T E L S G K C V V A L A						
927	ACA GAT CCC AAT ATC CTG AGC CTG AGT GGT AAG GTG CTG CCA TTC TGT GAC CTT	936	945	954	963	972
T D P N I L S L S G K V L P S C D L						
981	GCT CGA CGC TAT GGC CTT CGG GAT CTG GAC GGC CGC CCC GTG CAA GAC TAT TTG	990	999	1008	1017	1026
A R R Y G L R D V D G R P V Q D Y L						

Figure 1C

1035 1044 1053 1062 1071 1080  
 TCT TTG AGC TCT GTT CTC TCA CAC GTG TCC GGC CTG GGC TGG CTG GCC TCC TAC  
 S L S S V L S H V S G L G W L A S Y

1089 1098 1107 1116 1125 1134  
 CTG CCC TCC TTC CTC CGT GTG CCC AAG TGG ATT ATT GCC CTC TAC ACT AGC AAG  
 L P S F L R V P K W I A L Y T S K

1143 1152 1161 1170 1179 1188  
 TTC TAA CCC TCC TGG TCT GAC ACT ACG TCT CTG CTT GTC TTC TCA TTT GGA CTT  
 F

1197 1206 1215 1224 1233 1242  
 GGT GGT TCG TCC TGT CTC AGT GAA ACA GCA GCC TTT CTT GTT TAC CCA TAC CCT

1251 1260 1269 1278 1287 1296  
 TGA TAT GAA GAG AAG CCC TCT GCT GTG TGT CCG TGG TGA GTT CTG GGG TGC GCC

1305 1314 1323 1332 1341 1350  
 TAG GTC CCT TCT TTG TGC CTT GGT TTT CCT TGT CCT TCT TTT TAC TTT TTG CCT

1359 1368 1377 1386  
 TAG TAT TGA AAA ATG CTC TTG GAG CTA ATA AAA GTC TA 3'

Figure 1D

1 MAAPMNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRH 356351  
 1 MGVIQLQVAVLTGASRGIGRGIALQLGEAGATVYITGR R GI 2315796  
 41 - - - - - LDTLRVVAQEAQSLGGQCVPVVCDSSQES E 356351  
 41 PELSDNFRGLPSLDYVAKETISRGGKGIALLYVDHISNMT E GI 2315796  
 71 VRTLFEQVDR EQGRLDVLVNNAYAGVQTILNTRNKAFWE 356351  
 81 VKFLFEKIKEDEEGKLDILVNNVYNSLGKATEMI GKTFFD GI 2315796  
 111 TPASMWDDINNVLGRGHYFCSVYGARLMMVERRKGLIVNVG 356351  
 121 QDPSFWDDINGVGLRNHYFCSVYARMMVERRKGLIVNVG GI 2315796  
 151 SPGSLQYMFNVPGYGVGKAAACDKLAADCAHELRHGVSCVS 356351  
 161 SLGGLKYVFNVAYGAGKEALARMSTDMAVELNPNVVCVVT GI 2315796  
 191 LMPGIVQTELLKEHMAKEE - - - - - VLQDPVLKQFKSAFSSAE 356351  
 201 LIIPGPVKTE TANRTIIDDAYKMIKENPELEEF - - - - - IKGE GI 2315796  
 228 TTELSGKCVVALLATDPNILLSLGGKVLPSCDLARRYGLRDV 356351  
 237 STEYTGKALARLAMDPGKLKKGKTLFTEDLAQKYDFS D K GI 2315796  
 268 DGRPV - - - QDYLSLSSVLSHVSGLGWLASYLPSFLRVPKW I 356351  
 277 HGA GMEPQNI RLSIRTLIGTMGKEE - VAKYIIPQIKL PKW V GI 2315796  
 306 IALYTSKF 356351  
 316 IWQSVNRF GI 2315796

Figure 2